



#7

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## SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> Method for identifying compounds that modulate sister chromatid separation

<130> 0652.2290001

<140> To be assigned

<141> Herewith

<150> EP 01 101 252.3

<151> 2001-01-19

<150> US 60/297,440

<151> 2001-06-13

<160> 12

<170> PatentIn Ver. 2.1

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<211> 6668

<212> DNA

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ggg ctg agc ctt cag gag atg cct gga gat gtc ccc ctg gcc cgc atc Gly Leu Ser Leu Gln Glu Met Pro Gly Asp Val Pro Leu Ala Arg Ile 1660 1665 1670	5163
cag cgc ctc ttt tcc ttc agg gct ttg gaa tct ggc cac ttc ccc cag Gln Arg Leu Phe Ser Phe Arg Ala Leu Glu Ser Gly His Phe Pro Gln 1675 1680 1685	5211
cct gaa aag gag agt ttc cag gag cgc ctg gct ctg atc ccc agt ggg Pro Glu Lys Glu Ser Phe Gln Glu Arg Leu Ala Leu Ile Pro Ser Gly 1690 1695 1700 1705	5259
gtg act gtg tgt gtg ttg gcc ctg gcc acc ctc cag ccc gga acc gtg Val Thr Val Cys Val Leu Ala Leu Ala Thr Leu Gln Pro Gly Thr Val 1710 1715 1720	5307
ggc aac acc ctc ctg ctg acc cgg ctg gaa aag gac agt ccc cca gtc Gly Asn Thr Leu Leu Thr Arg Leu Glu Lys Asp Ser Pro Pro Val 1725 1730 1735	5355
agt gtg cag att ccc act ggc cag aac aag ctt cat ctg cgt tca gtc Ser Val Gln Ile Pro Thr Gly Gln Asn Lys Leu His Leu Arg Ser Val 1740 1745 1750	5403
ctg aat gag ttt gat gcc atc cag aag gca cag aaa gag aac agc agc Leu Asn Glu Phe Asp Ala Ile Gln Lys Ala Gln Lys Glu Asn Ser Ser 1755 1760 1765	5451
tgt act gac aag cga gaa tgg tgg aca ggg cgg ctg gca ctg gac cac Cys Thr Asp Lys Arg Glu Trp Trp Thr Gly Arg Leu Ala Leu Asp His 1770 1775 1780 1785	5499
agg atg gag gtt ctc atc gct tcc cta gag aag tct gtg ctg ggc tgc Arg Met Glu Val Leu Ile Ala Ser Leu Glu Lys Ser Val Leu Gly Cys 1790 1795 1800	5547



tgg aag ggg ctg ctg ctg ccg tcc agt gag gag ccc ggc cct gcc cag	5595
Trp Lys Gly Leu Leu Leu Pro Ser Ser Glu Glu Pro Gly Pro Ala Gln	
1805 1810 1815	
gag gcc tcc cgc cta cag gag ctg cta cag gac tgt ggc tgg aaa tat	5643
Glu Ala Ser Arg Leu Gln Glu Leu Leu Gln Asp Cys Gly Trp Lys Tyr	
1820 1825 1830	
cct gac cgc act ctg ctg aaa atc atg ctc agt ggt gcc ggt gcc ctc	5691
Pro Asp Arg Thr Leu Leu Lys Ile Met Leu Ser Gly Ala Gly Ala Leu	
1835 1840 1845	
acc cct cag gac att cag gcc ctg gcc tac ggg ctg tgc cca acc cag	5739
Thr Pro Gln Asp Ile Gln Ala Leu Ala Tyr Gly Leu Cys Pro Thr Gln	
1850 1855 1860 1865	
cca gag cga gcc cag gag ctc ctg aat gag gca gta gga cgt cta cag	5787
Pro Glu Arg Ala Gln Glu Leu Leu Asn Glu Ala Val Gly Arg Leu Gln	
1870 1875 1880	
ggc ctg aca gta cca agc aat agc cac ctt gtc ttg gtc cta gac aag	5835
Gly Leu Thr Val Pro Ser Asn Ser His Leu Val Leu Val Leu Asp Lys	
1885 1890 1895	
gac ttg cag aag ctg ccg tgg gaa agc atg ccc agc ctc caa gca ctg	5883
Asp Leu Gln Lys Leu Pro Trp Glu Ser Met Pro Ser Leu Gln Ala Leu	
1900 1905 1910	
cct gtc acc cgg ctg ccc tcc ttc cgc ttc cta ctc agc tac tcc atc	5931
Pro Val Thr Arg Leu Pro Ser Phe Arg Phe Leu Leu Ser Tyr Ser Ile	
1915 1920 1925	
atc aaa gag tat ggg gcc tcg cca gtg ctg agt caa ggg gtg gat cca	5979
Ile Lys Glu Tyr Gly Ala Ser Pro Val Leu Ser Gln Gly Val Asp Pro	
1930 1935 1940 1945	
cga agt acc ttc tat gtc ctg aac cct cac aat aac ctg tca agc aca	6027
Arg Ser Thr Phe Tyr Val Leu Asn Pro His Asn Asn Leu Ser Ser Thr	
1950 1955 1960	
gag gag caa ttt cga gcc aat ttc agc agt gaa gct ggc tgg aga gga	6075
Glu Glu Gln Phe Arg Ala Asn Phe Ser Ser Glu Ala Gly Trp Arg Gly	
1965 1970 1975	
gtg gtt ggg gag gtg cca aga cct gaa cag gtg cag gaa gcc ctg aca	6123
Val Val Gly Glu Val Pro Arg Pro Glu Gln Val Gln Glu Ala Leu Thr	
1980 1985 1990	
aag cat gat ttg tat atc tat gca ggg cat ggg gct ggt gcc cgc ttc	6171
Lys His Asp Leu Tyr Ile Tyr Ala Gly His Gly Ala Gly Ala Arg Phe	
1995 2000 2005	
ctt gat ggg cag gct gtc ctg cgg ctg agc tgt cgg gca gtg gcc ctg	6219
Leu Asp Gly Gln Ala Val Leu Arg Leu Ser Cys Arg Ala Val Ala Leu	
2010 2015 2020 2025	
ctg ttt ggc tgt agc agt gcg gcc ctg gct gtg cat gga aac ctg gag	6267
Leu Phe Gly Cys Ser Ser Ala Ala Leu Ala Val His Gly Asn Leu Glu	
2030 2035 2040	
ggg gct ggc atc gtg ctc aag tac atc atg gct ggt tgc ccc ttg ttt	6315
Gly Ala Gly Ile Val Leu Lys Tyr Ile Met Ala Gly Cys Pro Leu Phe	

2045	2050	2055	
ctg ggt aat ctc tgg gat gtg act gac cgc gac att gac cgc tac acg			6363
Leu Gly Asn Leu Trp Asp Val Thr Asp Arg Asp Ile Asp Arg Tyr Thr			
2060	2065	2070	
gaa gct ctg ctg caa ggc tgg ctt gga gca ggc cca ggg gcc ccc ctt			6411
Glu Ala Leu Leu Gln Gly Trp Leu Gly Ala Gly Pro Gly Ala Pro Leu			
2075	2080	2085	
ctc tac tat gta aac cag gcc cgc caa gct ccc cga ctc aag tat ctt			6459
Leu Tyr Tyr Val Asn Gln Ala Arg Gln Ala Pro Arg Leu Lys Tyr Leu			
2090	2095	2100	2105
att ggg gct gca cct ata gcc tat ggc ttg cct gtc tct ctg cgg taa			6507
Ile Gly Ala Ala Pro Ile Ala Tyr Gly Leu Pro Val Ser Leu Arg			
2110	2115	2120	
ccccatggag ctgtcttatt gatgctagaa gcctcataac tgttctacct ccaaggttag			6567
atttaatcct taggataact cttttaaagt gattttcccc agtgttttat atgaaacatt			6627
tccttttgat ttaacctcag tataataaag atacatcatt t			6668
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Met Arg Ser Phe Lys Arg Val Asn Phe Gly Thr Leu Leu Ser Ser Gln			
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Lys Glu Ala Glu Glu Leu Leu Pro Asp Leu Lys Glu Phe Leu Ser Asn			
20	25	30	
Pro Pro Ala Gly Phe Pro Ser Ser Arg Ser Asp Ala Glu Arg Arg Gln			
35	40	45	
Ala Cys Asp Ala Ile Leu Arg Ala Cys Asn Gln Gln Leu Thr Ala Lys			
50	55	60	
Leu Ala Cys Pro Arg His Leu Gly Ser Leu Leu Glu Leu Ala Glu Leu			
65	70	75	80
Ala Cys Asp Gly Tyr Leu Val Ser Thr Pro Gln Arg Pro Pro Leu Tyr			
85	90	95	
Leu Glu Arg Ile Leu Phe Val Leu Leu Arg Asn Ala Ala Ala Gln Gly			
100	105	110	
Ser Pro Glu Val Thr Leu Arg Leu Ala Gln Pro Leu His Ala Cys Leu			
115	120	125	
Val Gln Cys Ser Arg Glu Ala Ala Pro Gln Asp Tyr Glu Ala Val Ala			
130	135	140	
Arg Gly Ser Phe Ser Leu Leu Trp Lys Gly Ala Glu Ala Leu Leu Glu			
145	150	155	160
Arg Arg Ala Ala Phe Ala Ala Arg Leu Lys Ala Leu Ser Phe Leu Val			

Glu Pro Leu Cys Gln His Leu Gly Leu Val Lys Pro Gly Thr Tyr Pro  
485 490 495

Glu	Val	Pro	Pro	Glu	Lys	Leu	His	Arg	Cys	Phe	Arg	Leu	Gln	Val	Glu	
			500					505					510			
Ser	Leu	Lys	Lys	Leu	Gly	Lys	Gln	Ala	Gln	Gly	Cys	Lys	Met	Val	Ile	
		515					520					525				
Leu	Trp	Leu	Ala	Ala	Leu	Gln	Pro	Cys	Ser	Pro	Glu	His	Met	Ala	Glu	
	530					535					540					
Pro	Val	Thr	Phe	Trp	Val	Arg	Val	Lys	Met	Asp	Ala	Ala	Arg	Ala	Gly	
545					550					555					560	
Asp	Lys	Glu	Leu	Gln	Leu	Lys	Thr	Leu	Arg	Asp	Ser	Leu	Ser	Gly	Trp	
				565					570					575		
Asp	Pro	Glu	Thr	Leu	Ala	Leu	Leu	Leu	Arg	Glu	Glu	Leu	Gln	Ala	Tyr	
			580					585					590			
Lys	Ala	Val	Arg	Ala	Asp	Thr	Gly	Gln	Glu	Arg	Phe	Asn	Ile	Ile	Cys	
		595					600					605				
Asp	Leu	Leu	Glu	Leu	Ser	Pro	Glu	Glu	Thr	Pro	Ala	Gly	Ala	Trp	Ala	
	610					615					620					
Arg	Ala	Thr	His	Leu	Val	Glu	Leu	Ala	Gln	Val	Leu	Cys	Tyr	His	Asp	
625					630					635					640	
Phe	Thr	Gln	Gln	Thr	Asn	Cys	Ser	Ala	Leu	Asp	Ala	Ile	Arg	Glu	Ala	
				645					650					655		
Leu	Gln	Leu	Leu	Asp	Ser	Val	Arg	Pro	Glu	Ala	Gln	Ala	Arg	Asp	Gln	
			660					665					670			
Leu	Leu	Asp	Asp	Lys	Ala	Gln	Ala	Leu	Leu	Trp	Leu	Tyr	Ile	Cys	Thr	
		675					680					685				
Leu	Glu	Ala	Lys	Ile	Gln	Glu	Gly	Ile	Glu	Arg	Asp	Arg	Arg	Ala	Gln	
	690					695					700					
Ala	Pro	Gly	Asn	Leu	Glu	Glu	Phe	Glu	Val	Asn	Asp	Leu	Asn	Tyr	Glu	
705					710					715					720	
Asp	Lys	Leu	Gln	Glu	Asp	Arg	Phe	Leu	Tyr	Ser	Asn	Ile	Ala	Phe	Asn	
				725					730					735		
Leu	Ala	Ala	Asp	Ala	Ala	Gln	Ser	Lys	Cys	Leu	Asp	Gln	Ala	Leu	Ala	
			740					745					750			
Leu	Trp	Lys	Glu	Leu	Leu	Thr	Lys	Gly	Gln	Ala	Pro	Ala	Val	Arg	Cys	
		755					760					765				
Leu	Gln	Gln	Thr	Ala	Ala	Ser	Leu	Gln	Ile	Leu	Ala	Ala	Leu	Tyr	Gln	
	770					775					780					
Leu	Val	Ala	Lys	Pro	Met	Gln	Ala	Leu	Glu	Val	Leu	Leu	Leu	Leu	Arg	
785					790					795					800	
Ile	Val	Ser	Glu	Arg	Leu	Lys	Asp	His	Ser	Lys	Ala	Ala	Gly	Ser	Ser	
				805					810					815		
Cys	His	Ile	Thr	Gln	Leu	Leu	Leu	Thr	Leu	Gly	Cys	Pro	Ser	Tyr	Ala	
				820				825					830			

Gln Leu His Leu Glu Glu Ala Ala Ser Ser Leu Lys His Leu Asp Gln  
 835 840 845  
 Thr Thr Asp Thr Tyr Leu Leu Leu Ser Leu Thr Cys Asp Leu Leu Arg  
 850 855 860  
 Ser Gln Leu Tyr Trp Thr His Gln Lys Val Thr Lys Gly Val Ser Leu  
 865 870 875 880  
 Leu Leu Ser Val Leu Arg Asp Pro Ala Leu Gln Lys Ser Ser Lys Ala  
 885 890 895  
 Trp Tyr Leu Leu Arg Val Gln Val Leu Gln Leu Val Ala Ala Tyr Leu  
 900 905 910  
 Ser Leu Pro Ser Asn Asn Leu Ser His Ser Leu Trp Glu Gln Leu Cys  
 915 920 925  
 Ala Gln Gly Trp Gln Thr Pro Glu Ile Ala Leu Ile Asp Ser His Lys  
 930 935 940  
 Leu Leu Arg Ser Ile Ile Leu Leu Leu Met Gly Ser Asp Ile Leu Ser  
 945 950 955 960  
 Thr Gln Lys Ala Ala Val Glu Thr Ser Phe Leu Asp Tyr Gly Glu Asn  
 965 970 975  
 Leu Val Gln Lys Trp Gln Val Leu Ser Glu Val Leu Ser Cys Ser Glu  
 980 985 990  
 Lys Leu Val Cys His Leu Gly Arg Leu Gly Ser Val Ser Glu Ala Lys  
 995 1000 1005  
 Ala Phe Cys Leu Glu Ala Leu Lys Leu Thr Thr Lys Leu Gln Ile Pro  
 1010 1015 1020  
 Arg Gln Cys Ala Leu Phe Leu Val Leu Lys Gly Glu Leu Glu Leu Ala  
 1025 1030 1035 1040  
 Arg Asn Asp Ile Asp Leu Cys Gln Ser Asp Leu Gln Gln Val Leu Phe  
 1045 1050 1055  
 Leu Leu Glu Ser Cys Thr Glu Phe Gly Gly Val Thr Gln His Leu Asp  
 1060 1065 1070  
 Ser Val Lys Lys Val His Leu Gln Lys Gly Lys Gln Gln Ala Gln Val  
 1075 1080 1085  
 Pro Cys Pro Pro Gln Leu Pro Glu Glu Glu Leu Phe Leu Arg Gly Pro  
 1090 1095 1100  
 Ala Leu Glu Leu Val Ala Thr Val Ala Lys Glu Pro Gly Pro Ile Ala  
 1105 1110 1115 1120  
 Pro Ser Thr Asn Ser Ser Pro Val Leu Lys Thr Lys Pro Gln Pro Ile  
 1125 1130 1135  
 Pro Asn Phe Leu Ser His Ser Pro Thr Cys Asp Cys Ser Leu Cys Ala  
 1140 1145 1150  
 Ser Pro Val Leu Thr Ala Val Cys Leu Arg Trp Val Leu Val Thr Ala



1490	1495	1500
Leu Arg Gly Ser Asp 1505	Gly Glu Asp Ser Ala 1510	Ser Gly Gly Lys Thr Pro 1515 1520
Ala Pro Gly Pro Glu 1525	Ala Ala Ser Gly Glu 1530	Trp Glu Leu Leu Arg Leu 1535
Asp Ser Ser Lys Lys 1540	Lys Leu Pro Ser Pro 1545	Cys Pro Asp Lys Glu Ser 1550
Asp Lys Asp Leu Gly 1555	Pro Arg Leu Gln Leu 1560	Pro Ser Ala Pro Val Ala 1565
Thr Gly Leu Ser Thr 1570	Leu Asp Ser Ile Cys 1575	Asp Ser Leu Ser Val Ala 1580
Phe Arg Gly Ile Ser 1585	His Cys Pro Pro Ser 1590 1595	Gly Leu Tyr Ala His Leu 1600
Cys Arg Phe Leu Ala 1605	Leu Cys Leu Gly His 1610	Arg Asp Pro Tyr Ala Thr 1615
Ala Phe Leu Val Thr 1620	Glu Ser Val Ser Ile 1625	Thr Cys Arg His Gln Leu 1630
Leu Thr His Leu His 1635	Arg Gln Leu Ser Lys 1640	Ala Gln Lys His Arg Gly 1645
Ser Leu Glu Ile Ala 1650	Asp Gln Leu Gln Gly 1655	Leu Ser Leu Gln Glu Met 1660
Pro Gly Asp Val Pro 1665	Leu Ala Arg Ile Gln 1670	Arg Leu Phe Ser Phe Arg 1675 1680
Ala Leu Glu Ser Gly 1685	His Phe Pro Gln Pro 1690	Glu Lys Glu Ser Phe Gln 1695
Glu Arg Leu Ala Leu 1700	Ile Pro Ser Gly Val 1705	Thr Val Cys Val Leu Ala 1710
Leu Ala Thr Leu Gln 1715	Pro Gly Thr Val Gly 1720	Asn Thr Leu Leu Thr 1725
Arg Leu Glu Lys Asp 1730	Ser Pro Pro Val Ser 1735	Val Gln Ile Pro Thr Gly 1740
Gln Asn Lys Leu His 1745	Leu Arg Ser Val Leu 1750	Asn Glu Phe Asp Ala Ile 1755 1760
Gln Lys Ala Gln Lys 1765	Glu Asn Ser Ser Cys 1770	Thr Asp Lys Arg Glu Trp 1775
Trp Thr Gly Arg Leu 1780	Ala Leu Asp His Arg 1785	Met Glu Val Leu Ile Ala 1790
Ser Leu Glu Lys Ser 1795	Val Leu Gly Cys Trp 1800	Lys Gly Leu Leu Leu Pro 1805
Ser Ser Glu Glu Pro 1810	Gly Pro Ala Gln Glu 1815	Ala Ser Arg Leu Gln Glu 1820

Leu Leu Gln Asp Cys Gly Trp Lys Tyr Pro Asp Arg Thr Leu Leu Lys  
 1825 1830 1835 1840  
 Ile Met Leu Ser Gly Ala Gly Ala Leu Thr Pro Gln Asp Ile Gln Ala  
 1845 1850 1855  
 Leu Ala Tyr Gly Leu Cys Pro Thr Gln Pro Glu Arg Ala Gln Glu Leu  
 1860 1865 1870  
 Leu Asn Glu Ala Val Gly Arg Leu Gln Gly Leu Thr Val Pro Ser Asn  
 1875 1880 1885  
 Ser His Leu Val Leu Val Leu Asp Lys Asp Leu Gln Lys Leu Pro Trp  
 1890 1895 1900  
 Glu Ser Met Pro Ser Leu Gln Ala Leu Pro Val Thr Arg Leu Pro Ser  
 1905 1910 1915 1920  
 Phe Arg Phe Leu Leu Ser Tyr Ser Ile Ile Lys Glu Tyr Gly Ala Ser  
 1925 1930 1935  
 Pro Val Leu Ser Gln Gly Val Asp Pro Arg Ser Thr Phe Tyr Val Leu  
 1940 1945 1950  
 Asn Pro His Asn Asn Leu Ser Ser Thr Glu Glu Gln Phe Arg Ala Asn  
 1955 1960 1965  
 Phe Ser Ser Glu Ala Gly Trp Arg Gly Val Val Gly Glu Val Pro Arg  
 1970 1975 1980  
 Pro Glu Gln Val Gln Glu Ala Leu Thr Lys His Asp Leu Tyr Ile Tyr  
 1985 1990 1995 2000  
 Ala Gly His Gly Ala Gly Ala Arg Phe Leu Asp Gly Gln Ala Val Leu  
 2005 2010 2015  
 Arg Leu Ser Cys Arg Ala Val Ala Leu Leu Phe Gly Cys Ser Ser Ala  
 2020 2025 2030  
 Ala Leu Ala Val His Gly Asn Leu Glu Gly Ala Gly Ile Val Leu Lys  
 2035 2040 2045  
 Tyr Ile Met Ala Gly Cys Pro Leu Phe Leu Gly Asn Leu Trp Asp Val  
 2050 2055 2060  
 Thr Asp Arg Asp Ile Asp Arg Tyr Thr Glu Ala Leu Leu Gln Gly Trp  
 2065 2070 2075 2080  
 Leu Gly Ala Gly Pro Gly Ala Pro Leu Leu Tyr Tyr Val Asn Gln Ala  
 2085 2090 2095



Arg Gln Ala Pro Arg Leu Lys Tyr Leu Ile Gly Ala Ala Pro Ile Ala  
                   2100                                  2105                                  2110

Tyr Gly Leu Pro Val Ser Leu Arg  
                   2115                                  2120

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<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

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<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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caactgtcca ctagttgggt cagg

24

<210> 5

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

gaattcta at acgactcact ataggatcca tgatccctga ggaagaactg actg

54

<210> 6

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

gaattcta at acgactcact ataggatcca tgtctgacgg ggaagactca gcctc

55

<210> 7

<211> 56

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 7

gaattctaatac gactcact ataggatcca tggattccag caagaagaag ctgccc 56

&lt;210&gt; 8

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;400&gt; 8

ttattaccgc agagagacag gcaagcc 27

&lt;210&gt; 9

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (6)...(6)

&lt;223&gt; 7-Amido-4-methylcoumarin

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: recognition site

&lt;400&gt; 9

Asp Arg Glu Ile Met Arg

1 5

&lt;210&gt; 10

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: peptide inhibitor

&lt;400&gt; 10

Ser Val Glu Gln Gly Arg

1 5

&lt;210&gt; 11

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (6)...(6)

&lt;223&gt; 7-Amido-4-methylcoumarin

<220>

<223> Description of Artificial Sequence: recognition site

<400> 11

Ser Phe Glu Ile Leu Arg  
1 5

<210> 12

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD\_RES

<222> (6)...(6)

<223> 7-Amido-4-methylcoumarin

<220>

<223> Description of Artificial Sequence: peptide inhibitor

<400> 12

Glu Trp Glu Leu Leu Arg  
1 5

<210> 13

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD\_RES

<222> (7)...(7)

<223> 7-Amido-4-methylcoumarin

<220>

<221> Description of Artificial Sequence: recognition site

<400> 13

Ser Phe Glu Ile Leu Arg Gly  
1 5